



PALM INTRANET

Day : Tuesday  
Date: 2/8/2005  
Time: 09:53:52

## Continuity Information for 09/378045

### Parent Data

09378045

is a continuation in part of 08883036

Which is a continuation in part of 08869852

Which is a continuation in part of 08829536

Which is a continuation in part of 08815255

Which is a continuation in part of 08799861

### Child Data

No Child Data

Appln Info	Contents	Petition Info	Atty/Agent Info	Continuity Data	Foreign Data	Invent
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Search Another: Application#   or Patent#  PCT /  /   or PG PUBS #  Attorney Docket #  Bar Code #  

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Biotech/ChemLib

141188

From: Unknown@Unknown.com  
Sent: Thursday, December 23, 2004 3:01 PM  
To: STIC-Biotech/ChemLib  
Subject: Generic form response

ResponseHeader=Commercial Database Search Request

AccessDB#= \_\_\_\_\_

LogNumber= \_\_\_\_\_

Searcher= \_\_\_\_\_

SearcherPhone= \_\_\_\_\_

SearcherBranch= \_\_\_\_\_

MyDate=Thu Dec 23 15:01:02 EST 2004

submitto=Biotech01@uspto.gov

Name=Daniel Gamett

Empno=80545

Phone=2-1853

Artunit=1647

Office=REM4A44

Serialnum=09378045

PatClass=536

Earliest=Feb 13, 1997

Format1=paper

Format3=email

Searchtopic=The CRF is flawed for the pending case. Get the query sequence from the parent case, 08/883036.

Please do a standard search for SEQ ID NO:4, which is a peptide sequence.

Comments=M-F 8:30-5:00

send=SEND

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_

Searcher Phone: 2- \_\_\_\_\_

Date Searcher Picked up: 12/29/04

Date Completed: 12/29/04

Searcher Prep/Rev. Time: \_\_\_\_\_

Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_

AA Sequence: # 1

Structure: # \_\_\_\_\_

Bibliographic: \_\_\_\_\_

Litigation: \_\_\_\_\_

Patent Family: \_\_\_\_\_

Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_

DIALOG: \_\_\_\_\_

QUESTEL/ORBIT: \_\_\_\_\_

LEXIS/NEXIS: \_\_\_\_\_

SEQUENCE SYSTEM: 008

WWW/Internet: \_\_\_\_\_

Other(Specify): \_\_\_\_\_

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 29, 2004, 10:15:06 ; Search time 192 Seconds  
(without alignments)  
152.834 Million cell updates/sec

Title: US-08-883-036a-4  
Perfect score: 264  
Sequence: 1 ETRRCQCFDPAFLVFPDSWE.....EIKVAKAAAGHRDITLXTML 51

Scoring table: BIOSOM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues  
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	262	99.2	205	2	Q7Z218
2	262	99.2	411	2	Q6UXM8
3	262	99.2	411	2	AA088644
4	262	99.2	440	1	T10B_HUMAN
5	138	52.3	468	1	T10A_HUMAN
6	138	52.3	468	2	AAP35552
7	125	47.3	381	1	T10B_MOUSE
8	125	47.3	381	2	AAH65141
9	125	47.3	381	2	BAC37821
10	125	47.3	381	2	BAC37821
11	77	29.2	368	2	O57408
12	73.5	27.8	321	2	Q6DJ81
13	71	26.9	368	2	Q91AR7
14	71	26.9	368	2	Q9PW79
15	71	26.9	387	2	Q8VD70
16	71	26.9	413	2	Q99MM1
17	71	26.9	417	1	TR25_HUMAN
18	70	26.5	536	2	Q9FYW2
19	68.5	25.9	395	2	Q800K8
20	66.5	25.2	328	2	Q76B99
21	66.5	25.2	328	2	Q6GLZ4
22	66.5	25.2	328	2	BAD11770
23	66.5	25.2	372	2	Q9KJG7
24	65.5	24.8	471	1	TR1A_BOVIN
25	64	24.2	279	2	Q6BGC7
26	64	24.2	279	2	Q8NXP2
27	64	24.2	279	2	Q99VS0
28	63.5	24.1	279	2	Q7AEV6
29	63.5	23.9	156	2	DNT1_METKA
30	63.5	23.9	156	2	Q9LJF3
31	62.5	23.7	749	1	ACCG_MOUSE

32	62	23.5	1419	2	Q7R2Y7	Q7R2Y7 giardia lam
33	60.5	22.9	224	2	O01454	O01454 caenorhabdi
34	60.5	22.9	336	2	P91852	P91852 caenorhabdi
35	60	22.7	328	2	Q76B98	Q76B98 xenopus lae
36	60	22.7	328	2	BAD11771	BAD11771 xenopus l
37	59.5	22.5	1951	2	Q8DB34	Q8DB34 vibrio vuln
38	59.5	22.5	1954	2	Q7KIT8	Q7KIT8 vibrio vuln
39	59	22.3	144	1	CSF2_HUMAN	F04141 homo sapien
40	59	22.3	144	1	CSF2_SHEEP	P28773 ovine aries
41	59	22.3	279	2	Q6G1T9	Q6G1T9 staphylococ
42	59	22.3	332	1	HEM2_PROFR	P77923 propionibac
43	59	22.3	1893	2	Q8N377	Q8N377 emericella
44	58.5	22.2	362	2	Q915B8	Q915B8 pseudomonas
45	58	22.0	1022	2	Q9LDB8	Q9LDB8 arabidopsis

## ALIGNMENTS

RESULT 1	Q7Z218	PRELIMINARY;	PRT;	205 AA.
AC	Q7Z218			
DT	01-OCT-2003 (TREMBlrel. 25, Created)			
DT	01-OCT-2003 (TREMBlrel. 25, Last sequence update)			
DT	05-JUN-2004 (TREMBlrel. 27, Last annotation update)			
DE	Hypothetical protein DKFZp686A24188 (Hypothetical protein			
DE	DKFZp686B23188)			
GN	Name=DKFZp686A24188; Synonyms=DKFZp686B23188;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Human esophagus tumor;			
RA	Lauber J., Bahr A., Mewes H.W., Well B., Amid C., Osanger A., Fobo G.,			
RA	Han M., Wiemann S.;			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BX538179; CAD97801.1; -			
DR	EMBL; BX538179; CAD98053.1; -			
DR	GO; GO:0007165; P:signal transduction; IEA.			
DR	InterPro; IPR000488; Death.			
DR	Pfam; PF00531; Death; 1.			
DR	SMART; SM00005; DEATH; 1.			
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.			
KW	Hypothetical protein.			
SC	SEQUENCE 205 AA; 22612 MW; 34965B14AFC0313F CRC64;			
Query Match	99.2%;	Score 262;	DB 2;	Length 205;
Best Local Similarity	98.0%;	Pred. No. 2.3e-25;		
Matches	50;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	1 ETRRCQCFDPAFLVFPDSWEPLMKRLGIMDNEIKVAKAAAGHRDITLXTML 51			
DB	101 ETRRCQCFDPAFLVFPDSWEPLMKRLGIMDNEIKVAKAAAGHRDITLXTML 151			
RESULT 2				
AC	Q6UXM8	PRELIMINARY;	PRT;	411 AA.
DT	05-JUN-2004 (TREMBlrel. 27, Created)			
DT	05-JUN-2004 (TREMBlrel. 27, Last sequence update)			
DT	05-JUN-2004 (TREMBlrel. 27, Last annotation update)			
DE	TNFRSF10B/DR5.			
GN	ORFNames=UNQ160;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			

[7] SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.  
 RX MEDLINE=98090092; PubMed=9430227;  
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.,  
 RT "Death receptor 5, a new member of the TNFR family, and DR4 induce  
 RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
 RL Immunity 7:821-830(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANT LEU-32.  
 RX MEDLINE=97390509; PubMed=9242611;  
 RA Sheridan J.P., Maresters S.A., Pilti R.M., Gurney A., Skubatch M.,  
 RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,  
 RA "Control of TRAIL-induced apoptosis by a family of signaling and decoy  
 RT receptors.";  
 RL Science 277:818-821(1997).  
 RN [9]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANTS LEU-32 AND VAL-67.  
 RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yusa Y.,  
 RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2  
 RT gene in colorectal carcinoma.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RA Cao X., Zhang W., Wan T.,  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANTS LEU-32 AND VAL-67.  
 RA Farrar T., Yu T., Gilbert T., Gross J., O'Hara P.,  
 RT "Homo sapiens homolog of tumor necrosis factor receptor.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT LEU-32.  
 RC TISSUE=Gravid;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M., Uvedin T.B., Toshilyuk S., Carninci P., Prange C.,  
 RA Rana S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.O., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schmeich A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [13]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANTS LEU-32 AND VAL-67.  
 RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;  
 RA Hillman R.T., Green R.E., Brenner S.E.,  
 RT "An unappreciated role for RNA surveillance.";  
 RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.  
 RX MEDLINE=20017054; PubMed=10549288;  
 RA Hymanowicz S.G., Christinger H.W., Fuh G., Ulsch M., O'Connell M.,  
 RA Kelley R.F., Ashkenazi A., de Vos A.M.,  
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a  
 RT complex with death receptor 5.";  
 RL Mol. Cell 4:563-571(1999).  
 RN [15]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.  
 RX PubMed=10542098; DOI=10.1038/14935;  
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,

RA Jones E.Y., Screaton G.R.,  
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
 RT specificity in apoptotic initiation.";  
 RL Nat. Struct. Biol. 6:1048-1053(1999).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The  
 CC adaptor molecule FADD recruits caspase-8 to the activated  
 CC receptor. The resulting death-inducing signaling complex (DISC)  
 CC performs caspase-8 proteolytic activation which initiates the  
 CC subsequence cascade of caspases (aspartate-specific cysteine  
 CC proteases) mediating apoptosis. Promotes the activation of NF-  
 CC kappa-B.  
 CC -1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=long; Synonyms=TRICK29;  
 CC IsoId=O14763-1; Sequence=Displayed;  
 CC Note=May be produced at very low levels due to a premature stop  
 CC codon in the mRNA, leading to nonsense-mediated mRNA decay;  
 CC IsoId=O14763-2; Sequence=VSP\_006490;  
 CC Note=May be produced at very low levels due to a premature stop  
 CC codon in the mRNA, leading to nonsense-mediated mRNA decay;  
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;  
 CC very highly expressed in tumor cell lines such as Hela S3, K562,  
 CC HU-60, SW480, A549 and G361, highly expressed in heart, peripheral  
 CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,  
 CC ovary, uterus, placenta, testis, esophagus, stomach and throughout  
 CC the intestinal tract; not detectable in brain.  
 CC -1- INDUCTION: TNFSF10B is regulated by the tumor suppressor p53.  
 CC -1- DISEASE: Defects in TNFSF10B may be a cause of squamous cell  
 CC carcinoma of the head and neck (HNSCC) [MIM:601400].  
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 CC -----  
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 CC -----  
 DR EMBL: AF016849; AAC51778.1; -;  
 DR EMBL: AF018657; AAB70577.1; -;  
 DR EMBL: AF018658; AAB70578.1; -;  
 DR EMBL: AF016286; AAB81180.1; -;  
 DR EMBL: AF022386; AAB71949.1; -;  
 DR EMBL: AF012628; AAB67109.1; -;  
 DR EMBL: AF020501; AAB71412.1; -;  
 DR EMBL: AF016268; AAC01565.1; -;  
 DR EMBL: AF012535; AAB67103.1; -;  
 DR EMBL: AB014718; BAA33723.1; JOINED.  
 DR EMBL: AB014710; BAA33723.1; JOINED.  
 DR EMBL: AB014712; BAA33723.1; JOINED.  
 DR EMBL: AB014713; BAA33723.1; JOINED.  
 DR EMBL: AB014714; BAA33723.1; JOINED.  
 DR EMBL: AB014715; BAA33723.1; JOINED.  
 DR EMBL: AB014716; BAA33723.1; JOINED.  
 DR EMBL: AB014717; BAA33723.1; JOINED.  
 DR EMBL: AF153687; AAF75587.1; -;

Query Match 99.2%; Score 262; DB 1; Length 440;  
 Best Local Similarity 96.0%; Pred. No. 5.2e-25;  
 Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 ETRQCFDDPFDVLPFPDSWEPIAKKLGIMNDNEIKVAKAEAAAGHRDILXTM 51  
 Db 336 ETLQCFDDPFDVLPFPDSWEPIAKKLGIMNDNEIKVAKAEAAAGHRDILYTM 386

RESULT 5

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DT 02-MAR-2004 (T-EMBLrel. 27, last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, last annotation update)
DE Tumor necrosis factor receptor superfamily, member 10a.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaindl N., Chen X., Rolfe A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Laber J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
RT vector."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BI006906; AAPP552.1; -.
KW RECEPTOR.
SQ SEQUENCE 468 AA; 50061 MW; 7E9661859A550CD4 CRC64;

Query Match 52.3%; Score 138; DB 2; Length 468;
Best Local Similarity 56.9%; Pred. No. 5.1e-09;
Matches 23; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 1 ETLRQCFDDFADLVFPDSWEPIMRKLGIMDNEIKVAKAAGHRDTLXTML 51
Db 362 ETLMLFPDKRANIVFPDSMDQMRQLDTKNEIDVVRAGTAGPDALYAML 412

RESULT 7
T10B MOUSE STANDARD; PRT; 381 AA.
ID T10B_MOUSE: O9JUL5; O9JUL6;
AC O9JUL5: 28-FEB-2003 (Rel. 41, Created)
AC O9JUL6: 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 10B precursor (death
DE receptor 5) (MK).
OS Name=Tnftr10b; Synonyms=DS5, KILLER;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Kidney; PubMed=10383128;
RA MEDLINE=99310501;
RA Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.;
RT "Molecular cloning and functional analysis of the mouse homologue of
RT the KILLER/DS5 tumor necrosis factor-related apoptosis-inducing ligand
RT (TRAIL) death receptor."
RT Cancer Res. 59:2770-2775(1999).
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RA Nakamura Y., Tamari M., Watanabe O.;
RA "Mouse TRAIL receptor."
RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The
CC adaptor molecule FADD recruits caspase-8 to the activated
CC receptor. The resulting death-inducing signaling complex (DISC)
CC performs caspase-8 proteolytic activation which initiates the
CC subsequent cascade of caspases (aspartate-specific cysteine
CC proteases) mediating apoptosis. Promotes the activation of NF-
CC kappa-B.
CC -1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in heart, lung and kidney.
CC -1- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.
CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC -----
DR EMBL; AF176833; AAD52656.1; -.
DR EMBL; AB031081; BAA96462.1; -.
DR EMBL; AB031082; BAA96463.1; -.
DR HSSP; Q14763; 1DU3.
DR MGD; MGI:1341090; Tnftr10b.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_1like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Apoptosis; Receptor; Repeat; Signal; Transmembrane.
FT CHAIN 53 381
FT SIGNAL 1 52
FT DOMAIN 53 160
FT TRANSMEM 161 181
FT DOMAIN 182 381
FT REPEAT 26 86
FT REPEAT 87 129
FT REPEAT 130 169
FT DOMAIN 273 356
FT DISULFID 74 85
FT DISULFID 88 105
FT DISULFID 108 121
FT DISULFID 111 129
FT DISULFID 131 145
FT DISULFID 148 161
FT DISULFID 151 169
FT CONFLICT 42 42
FT CONFLICT 97 97
FT CONFLICT 128 128
FT CONFLICT 180 180
FT CONFLICT 187 187
FT CONFLICT 215 215
FT CONFLICT 229 229
FT CONFLICT 306 306
SQ SEQUENCE 381 AA; 42223 MW; 2F7999EA2EB485B1 CRC64;

Query Match 47.3%; Score 125; DB 1; Length 381;
Best Local Similarity 49.0%; Pred. No. 1.9e-07;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ETLRQCFDDFADLVFPDSWEPIMRKLGIMDNEIKVAKAAGHRDTLXTML 51
Db 270 DDLKFEYCGDIVFPDSWNRIMRQLGLTDNIOGMVAETLVTEALYOML 320

RESULT 8
ID AAH65141 PRELIMINARY; PRT; 381 AA.
AC AAH65141;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DE Tumor necrosis factor receptor superfamily, member 10b.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.

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ID 08VD70      PRELIMINARY;      PRT: 387 AA.
AC 08VD70;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tnfref25 protein.
GN Name=Tnfref25;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dietchenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadiri T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N. A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017526; AAL17526.1; -.
DR HSSP; P19438; IICH.
DR MGD; MGI:1934667; Tnfref25.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death_1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
SQ SEQUENCE 387 AA; 41640 MW; F1664466BAD68D3 CRC64;

Query Match 26.9%; Score 71; DB 2; Length 387;
Best Local Similarity 37.2%; Pred. No. 1.8;
Matches 16; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

```

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QY 9 DPADLVPPDSWEPLMKIGIMDNEIKYAKAAAGHRDTLXTML 51
DB 307 DWMDAVPARRWKEFVRLTIGLREARIEAVEVEICFRDQOYEML 349

```

Search completed: December 29, 2004, 10:36:13  
 Job time : 195 secs

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 29, 2004, 10:26:16 ; Search time 40 Seconds  
(without alignments)  
122.676 Million cell updates/sec

Title: US-08-883-036A-4

Perfect score: 264  
Sequence: 1 ETRRQCDDPADLVFPDSWE.....EIKYAKAEAGHRTLTXTML 51

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: Pir1:.\*  
2: Pir2:.\*  
3: Pir3:.\*  
4: Pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	64	24.2	279	2 H89841	hypothetical prote
2	60.5	22.9	336	2 T21438	hypothetical prote
3	60.5	22.9	552	2 T25496	hypothetical prote
4	59	22.3	144	1 FOHUGM	granulocyte-macrop
5	59	22.3	144	2 JH0469	granulocyte-macrop
6	58.5	22.2	362	2 E83542	hypothetical prote
7	58	22.0	1022	2 T50928	calmodulin-binding
8	58	22.0	1643	1 RRMGNV	genome polypeptid
9	57	21.6	144	1 A61632	granulocyte-macrop
10	57	21.6	447	2 S53982	hypothetical prote
11	57	21.6	450	2 A45967	vitellinogenin - rai
12	57	21.6	1165	2 D59433	C. elegans protein
13	57	21.6	1659	2 UC4986	vitellinogenin precu
14	56.5	21.4	336	2 T33011	probable transpos
15	56.5	21.4	459	2 H89530	protein H28G03.4
16	56	21.2	780	1 S43859	ATPase - Sulfolobu
17	56	21.2	1022	2 T51257	calmodulin-binding
18	55.5	21.0	219	2 D88890	protein C16C5.12
19	55.5	21.0	355	2 T29944	hypothetical prote
20	55.5	21.0	364	2 B64766	yeast protein - Eac
21	55.5	21.0	364	2 H85532	hypothetical prote
22	55.5	21.0	364	2 D90682	hypothetical prote
23	55.5	21.0	610	2 AG0227	exonuclease ABC c
24	55	20.8	140	2 T28918	hypothetical prote
25	55	20.8	252	2 AE1302	probable phosphop
26	55	20.8	811	2 AB0015	aspartate kinase
27	55	20.8	935	2 T19011	hypothetical prote
28	55	20.8	2848	2 T32550	hypothetical prote
29	54.5	20.6	1538	2 B90924	probable ATP-depen

30	54.5	20.6	1538	2 F85772	ATP-dependent heli
31	54.5	20.6	1538	2 G64922	probable ATP-depen
32	54	20.5	135	2 T24892	hypothetical prote
33	54	20.5	216	2 G90456	hypothetical prote
34	54	20.5	251	2 T28281	hypothetical prote
35	54	20.5	252	2 AE1674	probable phosphop
36	54	20.5	345	2 C87288	hypothetical prote
37	54	20.5	412	2 H90244	pre mRNA splicing
38	54	20.5	518	2 S60176	regulatory protein
39	54	20.5	619	2 A56519	CD16 protein - hu
40	54	20.5	620	2 T02840	probable membrane
41	53.5	20.3	290	2 S66355	lectin-related ste
42	53.5	20.3	376	2 A82676	conserved hypotet
43	53.5	20.3	390	2 E97478	cycH protein [limp
44	53.5	20.3	390	2 AE2696	cycH protein [limp
45	53.5	20.3	528	2 E71525	probable ABC trans

## ALIGNMENTS

RESULT 1  
H89841 hypothetical protein SA0658 [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: H89841  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Og  
ma, A.; Mizutani, U.; Y.; Kodayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; MUID:21311952; PMID:11418146  
A:Accession: H89841  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-279 <KUR>  
A:Cross-references: UNIPROT:Q9YSV0; GB:BA000018; PID:g13700594; PIDN:BAB41891.1; GSPDE  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: SA0658  
C:Superfamily: aldehyde reductase

Query Match 24.2%; Score 64; DB 2; Length 279;  
Best Local Similarity 39.5%; Pred. No. 1.5;  
Matches 15; Conservative 6; Mismatches 15; Indels 2; Gaps 1;

QY 4 RQCFDDPADL--VPFDSWEPIARKGLMDNEIKYAKAE 39  
DB 170 QOELQFCRDHDIKVTAWMPIMRNRLGIDNPVIVKIAE 207

RESULT 2  
T21438 hypothetical protein F26H9.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T21438  
R:Baynes, C.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z19422  
A:Accession: T21438  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-336 <ML>  
A:Cross-references: UNIPROT:P91852; EMBL:Z81516; PIDN:CAB04201.1; GSPDB:GN00019; CESP:  
A:Experimental source: clone F26H9  
C:Genetics:  
A:Gene: CESP:F26H9.3  
A:Map position: 1  
C:Superfamily: Caenorhabditis transposon Tc1 hypothetical 32k protein  
Query Match 22.9%; Score 60.5; DB 2; Length 336;



```
RESULT 6
E83542
C/Species: Pseudomonas aeruginosa
C/Accession: E83542
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: E83542
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-362 <STO>
A/Cross-references: UNIPROT:O915B8; GB:AE004517; GB:AE004091; NID:g9946710; PIDN:AA0421
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA0821

Query Match 22.2%; Score 58.5; DB 2; Length 362;
Best Local Similarity 25.4%; Pred. No. 10;
Matches 16; Conservative 10; Mismatches 18; Indels 19; Gaps 2;

OY 1 ETLRQCFDDFADLV-PFDSW-----EPLMRKLGMDNEIKVAKAFA 41
Db 56 ESTLCQCFDEFERLAPHLTWLRBPAGOKPLTAVRTQPLREMGAMDEDDHLSFCYTS 115
OY 42 GHR 44
Db 116 GKK 118

RESULT 7
T50928
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
R/Buaboocha, T.; Zielinski, R.E.
Submitted to the EMBL Data Library, December 1999
A/Description: Isolation of cDNA and genomic DNA clones encoding a calmodulin-binding pr
A/Reference number: Z25280
A/Accession: T50927
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1022 <BUA>
A/Cross-references: UNIPROT:O9LD58; EMBL:AF217546; PIDN:AAF28347.1
A/Accession: T50928
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1022 <BU2>
A/Cross-references: EMBL:AF217547; PIDN:AAF28348.1
C/Genetics:
A/Introns: 99/3; 148/3; 412/1; 480/3; 550/1; 713/3; 856/1; 883/1; 946/3; 1006/2

Query Match 22.0%; Score 58; DB 2; Length 1022;
Best Local Similarity 34.3%; Pred. No. 38;
Matches 12; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

OY 17 DSWEPIMRKLGLMDNEIKVAKAFAAGHRTLTMTL 51
Db 531 DSIEPALRRGRRLDREIFIGAPSTGRSDILHVL 565

RESULT 8
RRMGNV
genome polypeptide - narciessus mosaic virus
N/Alternate names: RNA nucleoside transferase (RNA-directed); RNA replicase
N/Contents: RNA-directed RNA polymerase (EC 2.7.7.48)
```

```
C/Species: narciessus mosaic virus
C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C/Accession: UT0470
R/Zuidema, D.; Linthorst, H.J.M.; Huismans, M.J.; Asjes, C.J.; Bol, J.F.
J. Gen. Virol. 70, 267-276, 1989
A/Title: Nucleotide sequence of narciessus mosaic virus RNA.
A/Reference number: JT0470; MUID:89279206; PMID:2732689
A/Accession: JT0470
A/Molecule type: genomic RNA
A/Residues: 1-1643 <ZUI>
A/Cross-references: UNIPROT:P15095; GB:D13747; GB:D00405; NID:g222107; PIDN:BA02891.1
C/Superfamily: eggplant mosaic virus RNA-directed RNA polymerase
C/Keywords: ATP; nucleotide binding; nucleoside transferase; P-loop; RNA biosynthesis;
F;868-875/Region: nucleotide-binding motif A (P-loop)
F;931-936/Region: nucleotide-binding motif B
F;874/Binding site: ATP (Lys) #status predicted

Query Match 22.0%; Score 58; DB 1; Length 1643;
Best Local Similarity 36.7%; Pred. No. 66;
Matches 11; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

OY 8 DDFADLVPPDSWEPIMRKLGLMDNEIKVAK 37
Db 746 DSVADSLPMASWVNLQKHGFGKNGQDIAQ 775

RESULT 9
A61632
granulocyte-macrophage colony-stimulating factor precursor - sheep
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A61632
R/O'Brien, P.M.; Rothel, J.S.; Seow, H.F.; Wood, P.R.
Immunol. Cell Biol. 69, 51-55, 1991
A/Title: Cloning and sequencing of the cDNA for ovine granulocyte-macrophage colony-st
A/Reference number: A61632; MUID:91331592; PMID:1869289
A/Accession: A61632
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-144 <OMB>
A/Cross-references: UNIPROT:O9MYK4; GB:X55991; NID:g6983759; PIDN:CAA39463.1; PID:g698
A/Superfamily: granulocyte-macrophage colony-stimulating factor
F;1-17/Domain: signal sequence #status predicted <SIG>

Query Match 21.6%; Score 57; DB 1; Length 144;
Best Local Similarity 33.3%; Pred. No. 5.6;
Matches 8; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

OY 1 ETLRQCFDDFADLVPPDSWEPIMR 24
Db 121 KSFENLKDPLFIIPDCMEPRAK 144

RESULT 10
S53982
hypothetical protein 447 - actinophaga RP3
C/Species: actinophaga RP3
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C/Accession: S53982
R/Gabriel, K.; Schmidt, H.; Schmidt, U.; Rausch, H.
Nucleic Acids Res. 23, 58-63, 1995
A/Title: The actinophaga RP3 DNA integrates site-specifically into the putative tRNA (
A/Reference number: S53981; MUID:95175570; PMID:7870591
A/Accession: S53982
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-447 <GAB>
A/Cross-references: EMBL:X80661
C/Genetics:
A/Start codon: GTG

Query Match 21.6%; Score 57; DB 2; Length 447;
Best Local Similarity 37.5%; Pred. No. 20;
```

